

9 18 27 36 45 54
 5' NAG GAN GGT GGG CGG CCC ANG GGT CCA GAG CGC AGT TCG GGT CGG AGC TYC GWC

 63 72 81 90 99 108
 CAG GCT GCT GGT ACC TGC GTC CGC CCG GCG AGC AGG ACA GGC TGC TTT GGT TTG

 117 126 135 144 153 162
 TGA CCT CCA CGC AGG ACG GCC ATC CTC TCC AGA ATG AAG ATC TTC TTG CCA GTG
 M K I F L P V

 171 180 189 198 207 216
 CTG CTG GCT GCC CTT CTG GGT GTG GAG CGA GCC AGC TCG CTG ATG TGC TTC TCC
 L L A A L L G V E R A S S L M C F S

 225 234 243 252 261 270
 TGC TTG AAC CAG AAG AGC AAT CTG TAC TGC CTG AAG CCG ACC ATC TGC TCC GAC
 C L N Q K S N L Y C L K P T I C S D

 279 288 297 306 315 324
 CAG GAC AAC TAC TGC GTG ACT GTG TCT GCT AGT GCC GGC ATT GGG AAT CTC GTG
 Q D N Y C V T V S A S A G I G N L V

 333 342 351 360 369 378
 ACA TTT GGC CAC AGC CTG AGC AAG ACC TGT TCC CCG GCC TGC CCC ATC CCA GAA
 T F G H S L S K T C S P A C P I P E

 387 396 405 414 423 432
 GGC GTC AAT GTT GGT GTG GCT TCC ATG GGC ATC AGC TGC TGC CAG AGC TTT CTG
 G V N V G V A S M G I S C C Q S F L

 441 450 459 468 477 486
 TGC AAT TTC AGT GCG GCC GAT GGC GGG CTG CGG GCA AGC GTC ACC CTG CTG GGT
 C N F S A A D G G L R A S V T L L G

 495 504 513 522 531
 GCC GGG CTG CTG CTG AGC CTG WTG CCG GCC CTG CTG CCG TTT GGC CCC TGA 3'
 A G L L L S L X P A L L R F G P *

FIGURE 1

5'	9	18	27	36	45	54
	GTG ACC ATG AAG GCT GTG CTG CTT GCC CTG TTG ATG GCA GGC TTG GCC CTG CAG					
	V T M K A V L L A L L M A G L A L Q					
	63	72	81	90	99	108
	CCA GGC ACT GCC CTG CTG TGC TAC TCC TGC AAA GCC CAG GTG AGC AAC GAG GAC					
	P G T A L L C Y S C K A Q V S N E D					
	117	126	135	144	153	162
	TGC CTG CAG GTG GAG AAC TGC ACC CAG CTG GGG GAG CAG TGC TGG ACC GCG CGC					
	C L Q V E N C T Q L G E Q C W T A R					
	171	180	189	198	207	216
	ATC CGC GCA GTT GGC CTC CTG ACC GTC ATC AGC AAA GGC TGC AGC TTG AAC TGC					
	I R A V G L L T V I S K G C S L N C					
	225	234	243	252	261	270
	GTG GAT GAC TCA CAG GAC TAC TAC GTG GGC AAG AAG AAC ATC ACG TGC TGT GAC					
	V D D S Q D Y Y V G K K N I T C C D					
	279	288	297	306	315	324
	ACC GAC TTG TGC AAC GSC AGC GGG GCC CAT GCC CTG CAG CCG GCT GCC GCC ATC					
	T D L C N X S G A H A L Q P A A A A I					
	333	342	351	360	369	378
	CTT GCG CTG CTC CCT GCA CTC GGC CTG CTG CTC TGG GGA CCC GGC CAG CTA TAG					
	L A L L P A L G L L W G P G Q L *					
	387	396	405	414	423	432
	GCT CTG GGG GGC CCC GGT GCA GCC CAC ACT GGG TGT GGT GCC CCA AGG CCT CTG					
	A L G G P X A A H T G C G A P R P L					
	441	450	459	468	477	486
	TGS CAC TCC TMA CAG ACC TGG GCC CAG TGG GAG SCT GTC TCT NGG TTC CTG AGG					
	X H S X Q T W A Q W E X V S X F L R					

CAC ATC CT 3'
H I

FIGURE 2

1 M - - - - K I F L P V L L A A L L G V E R A S S L M C F scah-1
 1 M S A T S N M R V F L P V L L A A L L G M E Q V H S L M C F GI 434660
 1 M S T T S S M R V F S I V L Q A H L L G V E L V P S L I C S GI 1199651
 1 M - - - - K A V I L L A L L M A G L A L Q P G T A L I C Y scah-2
 1 M - - - - K A F L F A V L A A V L C V E R A H T L I C F GI 509840

 25 S C L N Q K S N L Y C L K P T I C S D Q D N Y C V T V S A S scah-1
 31 S C T D Q K N N I N C L W P V S C Q E K D H Y C I T L S A A GI 434660
 31 S C T H Q K S N I N P P W P V A C K D T G N Y C I M L F S A GI 1199651
 25 S C K A Q V S N E D C L Q V E N C T Q L G E Q C W T A R I R scah-2
 25 S C S D A S S N W A C L T P V K C A E N E H C V T T Y V G GI 509840

 55 A G I G N L V T F G H S L S K T C S P A C P I P E - G V N V scah-1
 61 A G F G N - V N L G Y T L N K G C S P I C P S E N V N L N L GI 434660
 61 V G F G N - V N L G Y T L N T G C S Q S C P H E N I N I N P GI 1199651
 55 A V - - G L L T V - - I S K G C S L N C V D D S O D V Y V V scah-2
 55 V G I G G - - K S G Q S I S K G C S P V C P S A G I N L - - GI 509840

 84 G V A S M G I S C C Q S F L C N F S A A D G G L R A S V T L scah-1
 90 G V A S V N S V C C Q S S F C N F S A A G L G L R A S I P L GI 434660
 90 G V A S V N S Y - - Q S S F C N F S N A C L GI 1199651
 80 G K K N I T - - C C D T D L C N X S G A H - A L Q P A A A I scah-2
 81 G I A A A S V Y C C D S F L C N I S G S S - S V K A S Y A V GI 509840

 114 L G A G L L L S L X P A L L R F G P scah-1
 120 L G L G L L L S L L - A L L Q L S P GI 434660
 109
 107 L A - - L L P A L G L L L W G P G Q L GI 1199651
 110 L A L G I L V S F V - Y V L R A R E scah-2
 GI 509840

Decoration 'Decoration #1': Box residues that match the Consensus exactly.

FIGURE 3

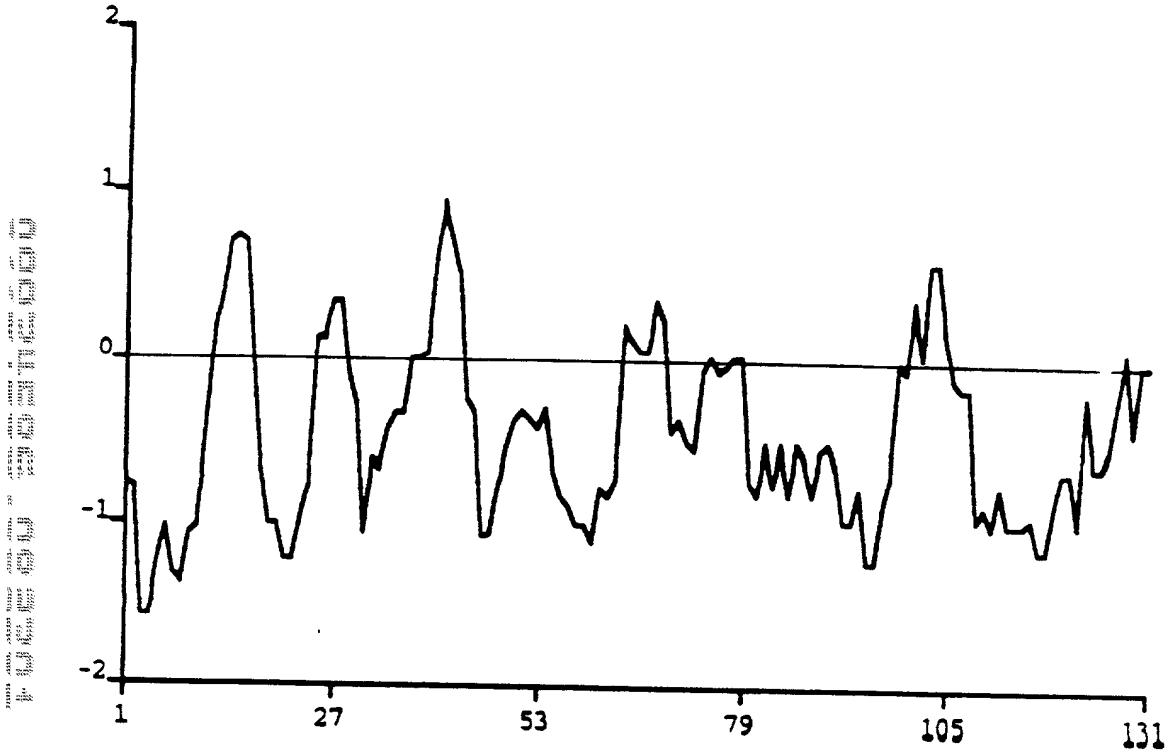


FIGURE 4

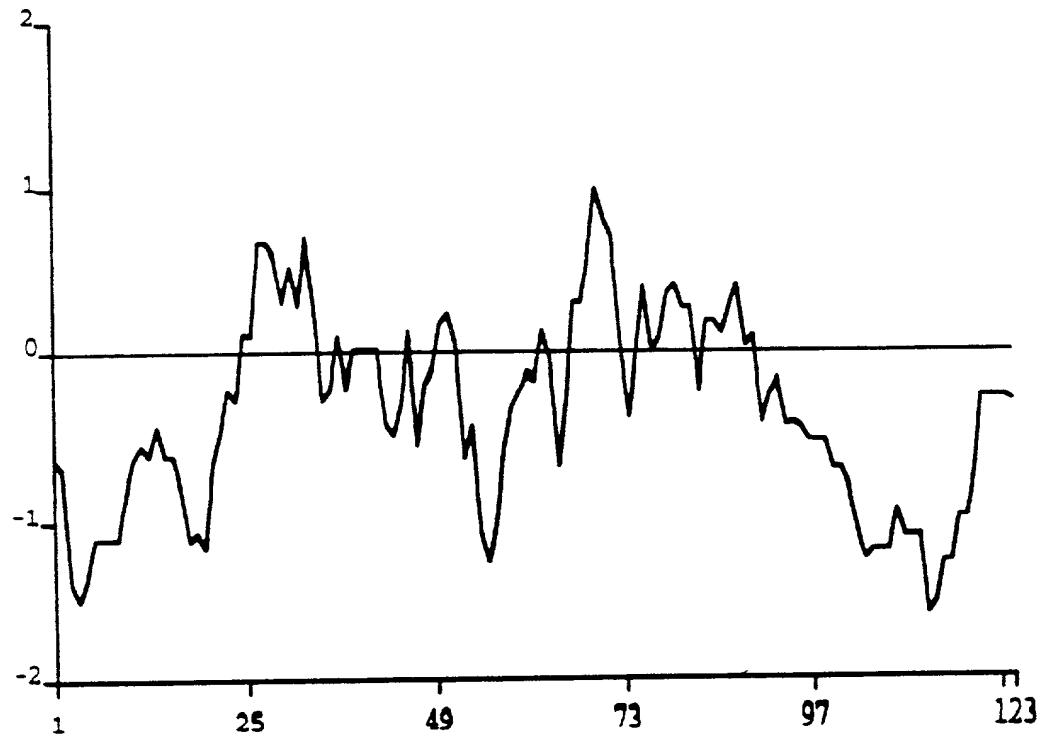


FIGURE 5

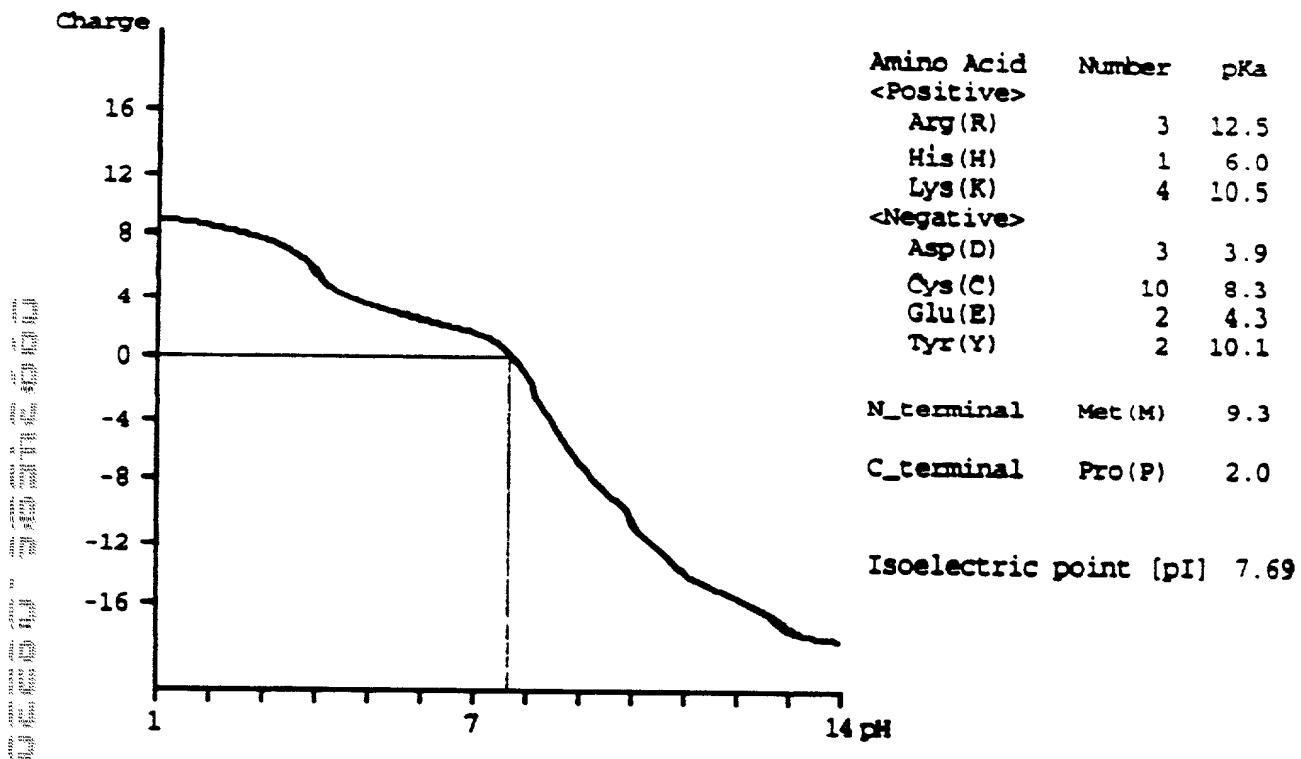


FIGURE 6

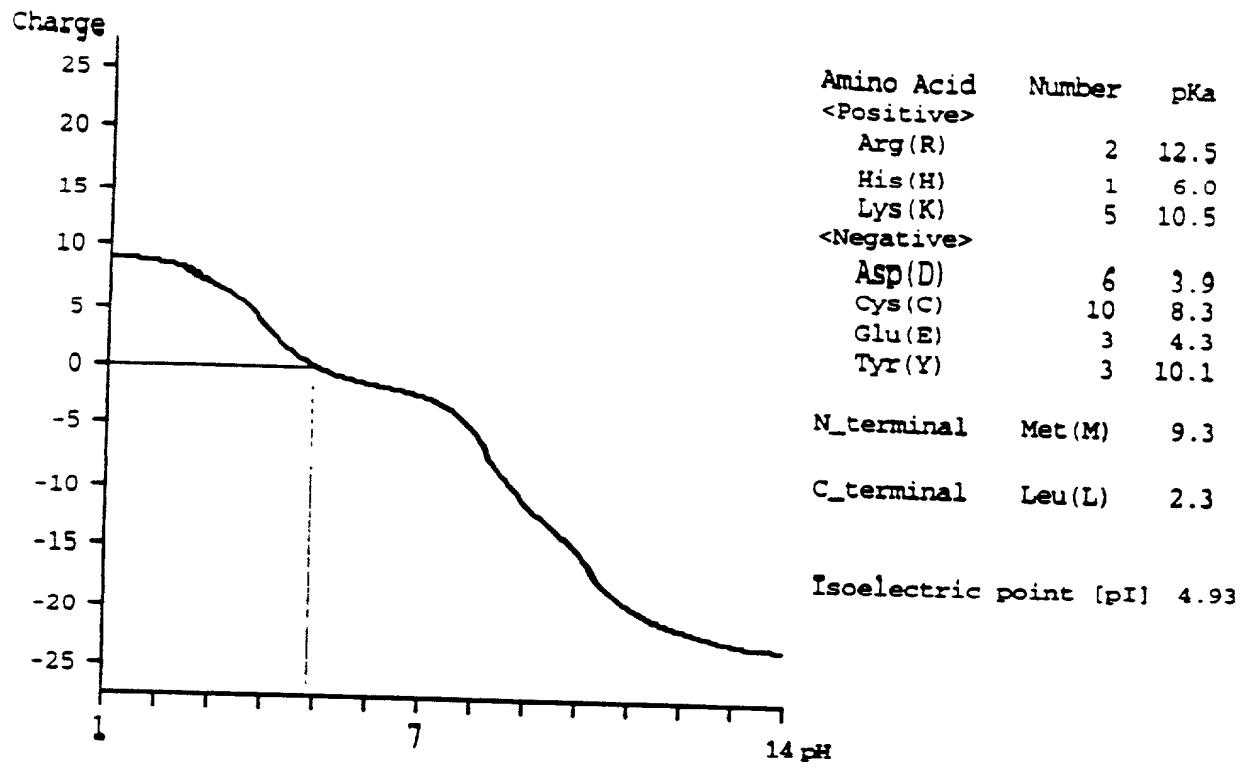


FIGURE 7